AMENDMENTS TO THE SPECIFICATION:

Please replace the paragraph bridging pages 5 and 6 (running from page 5, line 31, to page 6, line 13) with the following:

The present invention provides the means of identifying a plurality of organisms in a single sample without having to use multiple probes that are specific to each of the species and subspecies that might be present in the sample. The method uses universal primers, which are valid for identifying any species or subspecies present in the sample without prior knowledge of the organisms that might be present. According to the invention, a composition of universal primers are used, which hybridise with the conserved regions of the cytoplasmatic beta-actin gene, preferably with the sequences which lie between positions 1130-1191 and 1453-1473; 1453-1473 and 2041-2065; 2433-2459 and 2643-2680 and/or 26432680 and 2940-2960 (numbering in relation to the DNA sequence of the human locus HUMACCYBB Accession number M10277). The particular pairs of universal primers used are ~~P1~~ (1132-1151) 5'T000GCATGTGCAAGGCCGG3' **(SEQ ID NO: 1)** and ~~P2~~ (1474-1454) 5'CTCCATGTCGT000AGTTGG3' **(SEQ ID NO: 2)**; ~~P3~~ (1453-1484) 5'ACCAACTGGGACGACATGGAGAAGATCTGGC3' **(SEQ ID NO: 3)** and ~~P4~~ (2063-2034) 5'TACATGGCNGGGGTGTTAAAGGTCTCAAAC3' **(SEQ ID NO: 4)**, ~~P5~~ (2434-2463) 5'TGCCCTGAGGCCCTCTTCCAGCCTTCCTTC3' **(SEQ ID NO: 5)** and ~~P6~~

(2681-2643) 5'GGGTACATGGTGGTGCCGCCAGACAGCACNGTGTTGGC3' **(SEQ ID NO: 6)**; and ~~P7~~ (2643-2681) 5'GCCAACACNGTGCTGTCTGGCGGCACCACCATGTACCC3' **(SEQ ID NO: 7)** and ~~P8~~ (2952-2932) 5'TCGTACTCCTGCTTGCTGATCCACATCTG3' **(SEQ ID NO: 8)**.

Please replace the fourth full paragraph on page 7 (lines 19-27) with the following:

Figure 1 shows a diagram of the structure of the human cytoplasmatic beta-actin gene. The boxes represent the exons (exon 1 to 6) and the continuous black line represents the introns (I, Intron A to E). Regions W, X, Y and Z correspond to regions which lie between the pairs of primers **identified herein as SEQ ID NO: 1 and SEQ ID NO: 2, SEQ ID NO: 3 and SEQ ID NO: 4, SEQ ID NO: 5 and SEQ ID NO: 6, and SEQ ID NO: 7 and SEQ ID NO: 8,** ~~**P1 and P2, P3 and P4, P5 and P6, and, P7 and P8**~~ respectively. These fragments (W, X, Y and Z) include DNA sequences that are divergent between different biological species and can be amplified using PCR using primers **SEQ ID NO: 1 through SEQ ID NO: 8** ~~**P1 to P8**~~ as shown in figure 2.

Please replace the first full paragraph on page 8 (lines 16-32) with the following:

Figure 4 shows a diagram that illustrates the process of taxonomic identification proposed in this invention, using a biologically heterogeneous mixture. The biological sample is processed to extract the DNA and subject it to amplification by PCR. In the case that is illustrated here, the W region with primers **SEQ ID NO: 1 and SEQ ID NO: 2** ~~**P1 and P2**~~ is amplified. The PCR result is viewed using standard agarose gel electrophoresis (see electrophoresis gel, left-hand lane: molecular weight marker, 100 by ladder. Right-hand lane: bands (A and B, with approximate molecular weight expressed in base pairs bp, resulting from the PCR of the biological sample). The bands are isolated from the gel and are purified prior to undergoing DNA sequencing by standard methods. The DNA sequences obtained from each of the bands are used to interrogate a computer database that includes the sequences of the W region of biological species. The comparison of the sequences obtained using the existing sequences in the database gives the result of the identification of the species (or species) contained in the biological sample of origin.

Please replace the second full paragraph on page 9 (lines 19-33) with the following:

Figure 7 shows an experimental example of an agarose gel electrophoresis corresponding to ten separate amplifications by PCR of the W region which lies between primers **SEQ ID NO: 1 and SEQ ID NO: 2** ~~**P1 and P2**~~ of peripheral blood from eight different animal species. The numbers on each side indicate the approximate molecular weight, expressed in base pairs (bp), obtained for the W region in each of the amplifications. It is possible to observe the difference in molecular weight of this region between the animal species included. Oc: *Oryctolagus cuniculus*, rabbit. Cf: *Canis familiaris*, dog. Fc: *Felis catus, cat*. Us: *Ursus species*, Bear. Ec: *Equus caballus*, horse. Pt: *Pan troglodytes*, chimpanzee. Oa: *Ovis aries*, goat. Hs: *Homo sapiens*, man. The lanes on the left of the gel correspond to the 100 by ladder molecular weight standard (Invitrogen). In this standard, the lowest band corresponds to 100 by and as they ascend, each band is 100 by greater than the one immediately below it.

Please replace the third full paragraph on page 10 (lines 10-16) with the following:

The genome DNA obtained was then amplified by PCR. The W region (Figure 1) was amplified with the primers designed against nucleotide positions 1132-1151 (~~**P1,**~~ forward primer, 5'T000GCATGTGCAAGGCCGG3'**, SEQ ID NO: 1)** and 1474-1454 (~~**P2,**~~ reverse primer, 5'CTCCATGTCGTCCCAGTTGG3'**, SEQ ID NO: 2**), in accordance with

human sequence M10277. The PCR conditions were as follows: standard reagents, initial denaturation step at 94°C 3 minutes followed by 35 cycles of two steps each at 94°C 10 seconds and 68°C 2 minutes.

Please replace the fourth full paragraph on page 10 (lines 18-35) with the following:

The PCR result was viewed by standard horizontal agarose gel electrophoresis at 3% in TBE buffer. The bands that were obtained were compared with an Invitrogen 100 by ladder-marker molecular weight standard. Figure 4 shows the results that were obtained. The comparison of the mobility of the fragments amplified in the gel using the molecular weight marker shows a molecular weight of approximately 371 and 304 base pairs. If the molecular weights of the bands obtained are compared with a database of molecular sizes obtained a priori, it is possible to make a first approximation in identifying the species present in the starting sample. Figure 7 shows a pool of ten separate amplifications by PCR of the W region that lies between primers **SEQ ID NO: 1 and SEQ ID NO: 2** ~~**P1 and P2**~~ of peripheral blood from eight different animal species. It is possible to observe the difference in molecular weight of this region between the animal species included. Oc: *Oryctolagus cuniculus*, rabbit. Cf: *Canis familiaris*, dog. Fc: *Felis catus, cat.* Us: *Ursus species*, Bear. Ec: *Equus caballus*, horse. Pt: *Pan*

troglodytes, chimpanzee. Oa: *Ovis aries*, goat. Hs: *Homo sapiens*, man. The left-hand lanes of the gel correspond to the 100 by ladder molecular weight standard (Invitrogen). In a first approximation by comparison with this database of molecular weights, the bands obtained in figure 4 would correspond to goat (371 by band) and horse (304 by band).

In addition to the foregoing replacements, please amend the specification so to include, at the end of the specification and before the claims, the attached "Sequence Listing" consisting of three (3) pages.